

WHAT IS CLAIMED IS:

1. A method of preparing a transgenic cell having an altered transgene insertion comprising:
 - 5 a) obtaining a first transgenic cell, wherein the transgene insertion DNA sequence comprises a pre-selected DNA sequence flanked by directly repeated DNA sequences;
 - b) obtaining a plurality of progeny cells of any generation of the first transgenic cell;
 - 10 c) selecting a progeny transgenic cell wherein at least a portion of the transgene insertion is altered as compared to the first transgenic cell.
2. The method of claim 1, wherein said transgenic cell is a plant cell.
- 15 3. The method of claim 1, wherein said transgenic cell is homozygous for the transgene insertion DNA sequence.
4. The method of claim 1 wherein the pre-selected DNA sequence comprises a selectable marker gene or a reporter gene.
- 20 5. The method of claim 1 wherein the pre-selected DNA sequence further comprises a negative selectable marker gene.
6. The method of claim 5 wherein said negative selectable marker gene
25 comprises a *pehA* gene.
7. The method of claim 1 wherein the pre-selected DNA sequence comprises a *bar*, *nptII*, *EPSPS*, *GFP* or *cryIA(b)* gene.
- 30 8. A method of preparing a fertile transgenic plant having an altered transgene insertion comprising regenerating a plant from the progeny transgenic cell of claim 1.

A method of preparing a fertile transgenic plant having an altered transgene insertion comprising:

- a) obtaining a first transgenic plant, wherein the transgene insertion DNA sequence comprises a pre-selected DNA sequence flanked by directly repeated DNA sequences;
- b) obtaining a plurality of progeny of any generation of the first transgenic plant;
- c) selecting a progeny fertile transgenic plant wherein at least a portion of the transgene insertion is altered as compared to the first fertile transgenic plant.

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10. The method of claim 9, wherein said transgenic plant is homozygous for the transgene insertion DNA sequence.

11. The method of claim 9 wherein the pre-selected DNA sequence comprises a selectable marker gene or a reporter gene.

12. The method of claim 9 wherein the pre-selected DNA sequence comprises a bar, nptII, EPSPS or cryIA(b) gene.

13. The method of claim 9 wherein the plurality of progeny plants are obtained by self-pollination.

14. The method of claim 9 wherein the plurality of progeny plants are obtained by outcrossing to produce hybrid progeny.

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15. The method of claim 9 wherein the plurality of progeny plants are obtained by inbreeding to produce inbred plants.

16. The method of claim 9 wherein the plant is a monocot plant.

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17. The method of claim 16 wherein the monocot plant is a maize, barley, sorghum, wheat, rye or rice plant.

18. The method of claim 17 wherein the plant is a maize plant.

19. The method of claim 9 wherein the plant is a dicot plant.

5 20. The method of claim 19 wherein the dicot plant is a soybean, cotton, canola or potato plant.

21. The method of claim 9 wherein at least a portion of the transgene insertion is altered in that it has been deleted, amplified, or rearranged.

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22. A fertile transgenic plant produced by the method of claim 9.

23. The fertile transgenic plant of claim 22 which is inbred.

15 24. The fertile transgenic plant of claim 22 which is hybrid.

25. The fertile transgenic plant of claim 22 wherein the plant is a monocot plant.

26. The fertile transgenic plant of claim 25 wherein the monocot plant is a
20 maize, barley, wheat, sorghum, rye or rice plant.

27. The fertile transgenic plant of claim 26 wherein the plant is a maize plant.

28. The method of claim 21 wherein the plant is a dicot plant.

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29. The method of claim 28 wherein the plant is a soybean, cotton, canola or potato plant.

30. The fertile transgenic plant of claim 22 wherein at least a portion of the
30 transgene insertion is altered in that it has been deleted, amplified, or rearranged.

31. The fertile transgenic plant of claim 22 wherein at least a portion of the transgene insertion is altered in that it has been deleted.
32. The fertile transgenic plant of claim 22 wherein at least a portion of the transgene insertion is altered in that it has been amplified.
33. A seed produced by the fertile transgenic plant of claim 22
34. A fertile transgenic plant wherein at least a portion of a transgene insertion is altered from a parent transgene insertion.
35. The fertile transgenic plant of claim 34, wherein the plant is hybrid.
36. The fertile transgenic plant of claim 34, wherein the plant is inbred.
37. The fertile transgenic plant of claim 34, wherein at least a portion of the altered transgene insertion is altered in that it has been deleted, amplified, or rearranged.
38. The fertile transgenic plant of claim 34, wherein at least a portion of the altered transgene insertion is altered in that it has been deleted.
39. A progeny plant of any generation comprising an altered transgene insertion, wherein at least a portion of the transgene insertion is altered from the transgene insertion in a parental R0 plant.
40. An altered transgene insertion DNA sequence preparable by the method comprising:
- a) obtaining a first fertile transgenic plant comprising for a transgene insertion DNA sequence, wherein the transgene DNA sequence comprises a pre-selected DNA sequence flanked by directly repeated DNA sequences;

- b) obtaining a plurality of progeny of any generation of the first transgenic plant; and
- c) selecting a progeny fertile transgenic plant wherein at least a portion of the transgene insertion is altered as compared to the first fertile transgenic plant.

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41. The altered transgene insertion sequence of claim 40 wherein the first fertile transgenic plant is homozygous for the transgene insertion DNA sequence.

42. The altered transgene insertion of claim 40 wherein at least a portion of the
10 transgene insertion is altered in that it is deleted, amplified, or rearranged.

43. The altered transgene insertion of claim 40, wherein at least a portion of the transgene insertion is altered in that it has been deleted.

15 44. The altered transgene insertion of claim 40, wherein expression of a transgene contained within the parental transgene insertion is altered.

45. The altered transgene insertion of claim 40 where the alteration is identified by DNA analysis.

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46. The altered transgene insertion of claim 45 wherein the DNA analysis is by PCR.

47. The altered transgene insertion of claim 40 wherein the plant is a monocot
25 plant.

48. The altered transgene insertion of claim 47 wherein the monocot plant is a maize, barley, wheat, sorghum, rye or rice plant.

30 49. The altered transgene insertion of claim 48 wherein the plant is a maize plant.

50. The altered transgene insertion of claim 40 wherein the plant is a dicot plant.

51. The altered transgene insertion of claim 50 wherein the plant is a soybean, cotton, canola, or potato plant.

52. The altered transgene insertion of claim 50 wherein the plant is a soybean, cotton, canola, or potato plant.

53. The altered transgene insertion of claim 50 wherein the plant is a soybean, cotton, canola, or potato plant.